

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:37:25 ; Search time 1014.24 Seconds

(without alignments)
3608.645 Million cell updates/sec

Title: US-08-955-572-1
Perfect score: 838
Sequence: 1 atacagtttgcata atatggctgtggacttt 838

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

• total number of hits satisfying chosen parameters:

2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbL*

1: gb_ba1:*

2: gb_ba2:*

3: gb_om:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_p11:*

8: gb_p12:*

9: gb_pr1:*

10: gb_pr2:*

11: gb_pr3:*

12: gb_ro:*

13: gb_sy:*

14: gb_un:*

15: em_fun:*

16: em_hum1:*

17: em_hum2:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_v1:*

30: gb_ba3:*

31: gb_in1:*

32: gb_in2:*

33: gb_in3:*

34: gb_p13:*

35: gb_pr4:*

36: em_ba1:*

37: em_ba2:*

38: em_htg1:*

39: em_htg2:*

40: em_htg3:*

41: em_htg4:*

42: em_htg5:*

43: em_htg6:*

44: em_htg7:*

45: em_htg8:*

46: em_htg9:*

47: em_htg10:*

48: em_htg11:*

49: em_htg12:*

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56: em_htg19:*

57: em_htg20:*

58: em_htg21:*

59: em_htg22:*

60: em_htg23:*

61: em_hum3:*

62: em_hum4:*

63: em_hum5:*

64: em_hum6:*

65: gb_pr5:*

66: gb_pr6:*

67: gb_pr7:*

68: gb_htg1:*

69: gb_htg2:*

70: gb_htg3:*

71: gb_htg4:*

72: gb_htg5:*

73: gb_htg6:*

74: gb_htg7:*

75: gb_htg8:*

76: gb_htg9:*

77: gb_htg10:*

78: gb_htg11:*

79: gb_htg12:*

80: gb_htg13:*

81: gb_htg14:*

82: gb_htg15:*

83: gb_htg16:*

84: gb_htg17:*

85: gb_htg18:*

86: gb_htg19:*

87: gb_htg20:*

88: gb_htg21:*

89: gb_htg22:*

90: gb_htg23:*

91: gb_sts1:*

92: gb_sts2:*

93: gb_v1:*

94: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Lengt	DB	ID	Description
1	836.4	99.8	1415	5	168025		Sequence 7
2	836.4	99.8	1415	66	HS003397		U03397 Human receptor
3	836.4	99.8	1415	91	G28572		G28572 human STS
4	833.2	99.4	1419	67	L12964		L12964 Human activ
5	339.2	40.5	2350	12	J04492		J04492 Mouse T-cell
6	331.4	39.5	768	5	168024		168024 Sequence 5
c	144.8	17.3	65848	65	HS89183		AC025225 Human DNA
8	144.8	17.3	162975	78	AC025225		AC025225 Homo sapi
c	144.8	17.3	20773	78	AC025220		AC025220 Homo sapi
10	138	16.5	183941	88	AL365441		AL365441 Homo sapi
11	134.8	16.1	202773	78	AC025220		AC025220 Homo sapi
c	120.4	14.4	162975	78	AC025225		AC025225 Homo sapi

ALIGNMENTS

ORIGIN	ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Hominidae; Homo		
	1 (bases 1 to 1419)		
	Schwarz, H., Tuckwell, J. and Lotz, M.		
	A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor family		
	Gene 134 (2), 295-298 (1993)		
	94085/94		
	2 (bases 1 to 1419)		
	Schwarz, H.		
	Direct Submission		
	Submitted (22-APR-1993) Sam and Rose Stein Institute for Research		
	on Aging, University of California, San Diego, La Jolla, CA		
	92093-0663, USA		
	3 (bases 1 to 1419)		
	Schwarz, H.		
	Direct Submission		
	Submitted (05-MAR-1999) Sam and Rose Stein Institute for Research		
	on Aging, University of California, San Diego, La Jolla, CA		
	92093-0663, USA		
	Sequencing update by submitter		
	On Mar 5, 1999 this sequence replaced gi:292237.		
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	/note="ILA"		
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	140. 907		
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	/note="Induced by lymphocyte activation; similar to Human receptor protein encoded by GenBank Accession Number U03397"		
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	EDDCKGQDLETKGCKDQCFGTENDRGICREWTCNSDUGKSVLYNSTKERDVYCGP		
	SPADLSPSVPAPPAPRPGHSQPLISSEPLALSTIALFLFLFLTRFSVVKGRK		
	KLIVYIFKOPFMREVQTOBEDGSCRFPEEEGCCL"		
	3' UTR		
	908. 1419		
	/gene="CD137"		
	1369. 1374		
	/gene="CD137"		
	1419		
	/gene="CD137"		
	BASE COUNT		
	374 a 340 c 341 g 364 t		
	ORIGIN		
	Query Match	99.4%	Score 833.2; DB 67; Length 1419;
	Best Local Similarity	99.6%	Pred. No. 1e-244; Mismatches 3; Indels 0; Gaps 0;
	Matches	835; Conservative	
	polyA_signal		
	polyA_site		
	Query	1 aatcagctttcttagtatcatactctgtccagatttcataatggaaacgttgttacaa	
	Db	100 AATCAGCTTTCTAGTATCATACCTGTCAGATTTCATATGGAAACGTGTACAA	159
	RESULT	4	
	HUMILAX		
	LOCUS	1419 bp	mRNA
	DEFINITION	Human activation dependent T cell mRNA, complete cds.	PRI 05-MAR-1999
	ACCESSION	L12664	
	VERSION	L12664.2	GI: 4337126
	KEYWORDS	cell surface receptor; nerve growth factor receptor; human 4-1BB homolog; tumor necrosis factor receptor; CD137.	
	SOURCE	human	

/note="MIR repeat: matches 28. .218 of consensus"	repeat_region	15407. .15757
/note="AluSx repeat: matches 1. .312 of consensus"	repeat_region	15781. .16029
4115. .4375	repeat_region	16060. .16113
/note="AluSx repeat: matches 1. .245 of consensus"	repeat_region	/note="MIR repeat: matches 196. .250 of consensus"
4377. .4658	repeat_region	16126. .16159
/note="AluY repeat: matches 1. .291 of consensus"	repeat_region	/note="17 copies 2 mer ta 82% conserved"
4669. .4733	repeat_region	16167. .16222
/note="AluSx repeat: matches 232. .296 of consensus"	repeat_region	/note="28 copies 2 mer tg 71% conserved"
5240. .5454	repeat_region	16225. .16310
/note="AluY repeat: matches 39. .299 of consensus"	repeat_region	/note="MIR repeat: matches 120. .204 of consensus"
5455. .5888	repeat_region	16382. .16451
/note="L1M48 repeat: matches 5622. .6097 of consensus"	repeat_region	/note="L12 repeat: matches 1694. .1797 of consensus"
5889. .6147	repeat_region	16446. .16621
/note="AluSx repeat: matches 54. .312 of consensus"	repeat_region	/note="L2 repeat: matches 2260. .2417 of consensus"
6118. .6355	repeat_region	17192. .17311
/note="L1M48 repeat: matches 6097. .6289 of consensus"	repeat_region	/note="AluY repeat: matches 2. .126 of consensus"
6365. .6579	repeat_region	17580. .17953
/note="L1M22 repeat: matches 5869. .6086 of consensus"	repeat_region	/note="187 copies 2 mer cc 60% conserved"
6749. .7061	repeat_region	17625. .17954
/note="MIR1D repeat: matches 197. .505 of consensus"	repeat_region	/note="110 copies 3 mer cct 78% conserved"
7062. .7378	repeat_region	17986. .18200
/note="AluSx repeat: matches 1. .306 of consensus"	repeat_region	/note="AluSg repeat: matches 1. .293 of consensus"
7379. .7570	repeat_region	18808. .19052
/note="MIR1D repeat: matches 5. .197 of consensus"	repeat_region	/note="AluU repeat: matches 34. .306 of consensus"
7625. .7661	repeat_region	19215. .19517
/note="L12 repeat: matches 2638. .2709 of consensus"	repeat_region	/note="AluSx repeat: matches 119. .132 of consensus"
7823. .8112	repeat_region	19617. .19728
/note="AluU repeat: matches 1. .311 of consensus"	repeat_region	/note="MLT2B repeat: matches 1. .119 of consensus"
8714. .8755	repeat_region	19729. .20034
/note="21 copies 2 mer tt 76% conserved"	repeat_region	/note="AluSp repeat: matches 1. .308 of consensus"
8766. .9065	repeat_region	20035. .20048
/note="AluU repeat: matches 1. .309 of consensus"	repeat_region	/note="MLT2B repeat: matches 119. .132 of consensus"
9188. .9257	repeat_region	20049. .20127
/note="MER5A repeat: matches 10. .79 of consensus"	repeat_region	/note="MADE1 repeat: matches 1. .80 of consensus"
9292. .9530	repeat_region	20128. .20237
/note="AluSg repeat: matches 1. .290 of consensus"	repeat_region	/note="MLT2B repeat: matches 132. .279 of consensus"
9679. .9986	repeat_region	20298. .20609
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10829. .10912	repeat_region	20547
/note="L1 repeat: matches 4918. .5003 of consensus"	repeat_region	/note="match: GSS: Em:B75776"
10933. .10989	repeat_region	20993. .21102
/note="L1 repeat: matches 3505. .3562 of consensus"	repeat_region	/note="55 copies 2 mer aa 75% conserved"
11295. .11589	repeat_region	21561. .21859
/note="AluSg repeat: matches 1. .291 of consensus"	repeat_region	/note="AluSx repeat: matches 1. .299 of consensus"
11793. .12283	repeat_region	21958. .22249
/note="L1M4 repeat: matches 4475. .4848 of consensus"	repeat_region	/note="AluU repeat: matches 2. .299 of consensus"
12184. .12478	repeat_region	22472. .22611
/note="AluY repeat: matches 1. .292 of consensus"	repeat_region	/note="AluSg repeat: matches 1. .142 of consensus"
12479. .12806	repeat_region	22612. .22907
/note="L1M4 repeat: matches 4099. .4475 of consensus"	repeat_region	/note="AluSx repeat: matches 1. .301 of consensus"
12808. .13063	repeat_region	22908. .23072
/note="L1M42 repeat: matches 252. .495 of consensus"	repeat_region	/note="AluSg repeat: matches 142. .300 of consensus"
13064. .13333	repeat_region	23255. .23400
/note="AluY repeat: matches 36. .303 of consensus"	repeat_region	/note="THE1B repeat: matches 219. .364 of consensus"
13334. .13478	repeat_region	23401. .23682
/note="L1M2 repeat: matches 66. .252 of consensus"	repeat_region	/note="AluSC repeat: matches 1. .295 of consensus"
13479. .13851	repeat_region	23683. .23823
/note="MSR2 repeat: matches 1. .426 of consensus"	repeat_region	/note="THE1B repeat: matches 1. .220 of consensus"
13852. .13921	repeat_region	23868. .24164
/note="AluY repeat: matches 1. .66 of consensus"	repeat_region	/note="AluSx repeat: matches 14. .308 of consensus"
13922. .14007	repeat_region	repeat_region
/note="L1M4 repeat: matches 4017. .4102 of consensus"	repeat_region	Query Match 17.3%; Score 144.8; DB 65; Length 65848; Best Local Similarity 95.5%; Pred. No. 5.6e-33; Mismatches 149; Conservation 0; Indels 0; Gaps
14105. .14264	repeat_region	Qy 233 tgcaggcaggtaagggtgtttcaggccatggatgtttccaccaggatcgca 292
/note="AluY repeat: matches 314. .520 of consensus"	repeat_region	Db 52938 TGGGGGAACTGTGTTTCAGGGCACCAGGAAAGGTGTTCCACCAATGCCA 5287
14314. .14507	repeat_region	/note="MTRIF repeat: matches 144664)
/note="complement:14508 .14664)	misc_feature	/note="match: SRS: Em:AL034007"
14707. .15011	repeat_region	/note="AluY repeat: matches 1. .305 of consensus"
1507. .15385	repeat_region	/note="AluSx repeat: matches 1. .295 of consensus"
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 misc_feature /note="assembly_name:Contig30"
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 misc_feature 92544 . 103799
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 Best Local Similarity 95.5%; Pred. No. 6.5e-33;
 Matches 149; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 233 tgaggcagttaaagggtttcaggaccagaaggagtgtccacccaggaaatgca 292
 Db 90075 GAGGGGACTTTCAGGGTCTTCAGGACAGAGGACTGTCCTCCACAGCAATCA 90134
 Qy 293 gagtgtgactctccgggtttcactgctggggcaggatgcaggatgtgtggaaacag 352
 Db 90135 GAGTGTGCTGCACCTCCAGGGTTCACNGCTGGGGAGGATGCAATGTCAGACAG 90194
 Qy 353 gatgtaaacaaaggtaagaactgacaaaaaaagg 388
 Db 90195 GATGTAAACAAAGTCAGAACTGACAAAAAGGT 90230

RESULT 9
 AC025220/c LOCUS AC025220 202773 bp DNA 07-APR-2000
 DEFINITION Homo sapiens chromosome 1 clone RP11-281E22 map 1, WORKING DRAFT
 SEQUENCE 35 unordered pieces.
 ACCESSION AC025220
 VERSION AC025220.2 GI:7523798
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 Unpublished
 2 (bases 1 to 202773) Birren, B.; Linton, L.; Nusbaum, C. and Lander, E.
 TITLE
 AUTHORS Anderson, S.; Baldwin, J.; Barna, N.; Bastin, V.; Beda, F.;
 Boquilkowski, L.; Boukagalter, B.; Brown, A.; Burlett, G.;
 Campopiano, A.; Castle, A.; Choepel, Y.; Colangelo, M.; Collins, S.;
 Collymore, A.; Cooke, P.; Dearellano, K.; Dewar, K.; Diaz, J. S.;
 Dodge, S.; Domino, M.; Doyle, M.; Ferreira, P.; FitzHugh, W.; Gage, D.;
 Galagan, J.; Gardyne, S.; Ginde, S.; Goyette, M.; Graham, L.;

Grand-Pierre, N.; Grant, G.; Hagos, B.; Heaford, A.; Horton, L.;
 Howland, J.C.; Iliev, I.; Jones, C.; Kann, L.; Karatas, A.;
 Klein, J.; LaRocque, K.; Lamazares, R.; Landers, T.; Lehoczky, J.;
 Levine, R.; Lieu, C.; Liu, G.; Locke, K.; Macdonald, P.; Marquis, N.;
 McCarthy, M.; McEwan, P.; McFarland, K.; McFneeters, R.;
 Meldrum, J.; Menus, L.; Mihova, T.; Miranda, C.; Mlenga, V.; Morrow, J.;
 Murphy, T.; Naylor, J.; Norman, C. H.; O'Connor, T.; O'Donnell, P.;
 O'Neill, D.; Olivar, T.M.; Oliver, J.; Peter, C.; Pierre, N.;
 Pisani, C.; Pollara, V.; Raymond, C.; Riley, R.; Rogov, P.; Rothman, D.;
 Roy, A.; Santos, R.; Schauer, S.; Severy, P.; Spencer, B.;
 Stange-Rhomann, N.; Stojanovic, N.; Subramanian, A.; Talamas, J.;
 Tesfaye, S.; Theodore, J.; Turrell, A.; Travers, M.; Trigilio, J.;
 Vassiliev, H.; Viel, R.; Vo, A.; Wilson, B.; Wu, X.; Wyman, D.; Ye, W.J.;
 Young, G.; Zainoun, J.; Zimmer, A. and Zody, M.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Apr 7, 2000 this sequence version replaced gi:7188898.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A.; Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence@genome.wi.mit.edu
 ----- Project Information
 Center project name: L8035
 Center clone name: 281_E_22
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: dye-terminator; Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 182912 bases at least Q40
 Consensus quality: 192383 bases at least Q30
 Consensus quality: 195712 bases at least Q20
 Insert size: 1993/3; sum-of-contigs
 Quality coverage: 3.5 in Q20 bases; sum-of-contigs
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs
 ----- * NOTE: This is a 'working draft' sequence. It currently
 * consists of 35 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1182: contig of 1182 bp in length
 * 1183 1282: gap of 100 bp
 * 1283 2698: contig of 1416 bp in length
 * 2699 2798: gap of 100 bp
 * 2799 4194: contig of 1396 bp in length
 * 4195 4294: gap of 100 bp
 * 4295 5104: contig of 1410 bp in length
 * 5705 5804: gap of 100 bp
 * 5805 8389: contig of 2585 bp in length
 * 8390 8489: gap of 100 bp
 * 8490 10352: contig of 1863 bp in length
 * 10353 10452: gap of 100 bp
 * 10453 1304: contig of 2572 bp in length
 * 13025 13124: gap of 100 bp
 * 13125 15150: contig of 2585 bp in length
 * 15710 15809: gap of 100 bp
 * 15810 10352: contig of 1661 bp in length
 * 17471 17570: gap of 100 bp
 * 17571 20151: contig of 2581 bp in length
 * 20152 20251: gap of 100 bp
 * 20252 22970: contig of 2619 bp in length
 * 22871 22970: gap of 100 bp
 * 22971 25709: contig of 2739 bp in length
 * 25710 25809: gap of 100 bp

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 * 28339 28438: gap of 100 bp
 * 28439 32476: contig of 4038 bp in length
 * 32477 32576: gap of 100 bp
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 * 37519 37618: gap of 100 bp
 * 37619 41724: contig of 4106 bp in length
 * 41725 41824: gap of 100 bp
 * 41825 46408: contig of 4584 bp in length
 * 46409 46508: gap of 100 bp
 * 46509 51711: contig of 5203 bp in length
 * 51712 51811: gap of 100 bp
 * 51812 56660: contig of 5049 bp in length
 * 56861 56960: gap of 100 bp
 * 56961 62871: contig of 5911 bp in length
 * 62872 62971: gap of 100 bp
 * 62972 69111: contig of 6140 bp in length
 * 69112 69211: gap of 100 bp
 * 69212 75632: contig of 6421 bp in length
 * 75633 75732: gap of 100 bp
 * 75733 81565: contig of 5833 bp in length
 * 81566 81665: gap of 100 bp
 * 81666 88181: contig of 6516 bp in length
 * 88182 88281: gap of 100 bp
 * 88282 9593: contig of 7312 bp in length
 * 95594 95693: gap of 100 bp
 * 95694 103809: contig of 8116 bp in length
 * 103810 103909: gap of 100 bp
 * 103910 112398: contig of 8489 bp in length
 * 112399 112498: gap of 100 bp
 * 112499 120133: contig of 7535 bp in length
 * 120034 120133: gap of 100 bp
 * 120134 12904: contig of 8871 bp in length
 * 129005 129104: gap of 100 bp
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 * 146984 147093: gap of 100 bp
 * 147094 156907: contig of 9824 bp in length
 * 156908 157007: gap of 100 bp
 * 157008 168350: contig of 11343 bp in length
 * 168351 168450: gap of 100 bp
 * 168451 185312: contig of 16762 bp in length
 * 185213 185312: gap of 100 bp
 * 185313 202773: contig of 17461 bp in length.

FEATURES
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 /db_xref="taxon:9606"
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 Best Local Similarity 95..58%; Pred. No. 6..8e-33;
 Matches 149; Conservative 0; Mismatches 7; Indels 0; Gaps

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 DB 37982 TGGGGGAGCTTGTAGTGTCTTCAAGGAAAGGAGTGTCTCACCAAGCAATGCA 37922

QY 293 gagttggactcaactccagggttttcgtccggggcaggatgcacatgtgtgtacac 352
 DB 37922 GAGTGTGACTCCTACGGTTTCAGCTTCACTGGGCGAGTGCAGTGTGACAG 37863

QY 353 gattgttaaacaggtaaactgaaactgaaaaaaagggt 388
 DB 37862 GATTGTAACAGGTCAAGAAGTCAAAAGGT 37827

RESULT 10
 AL365441 LOCUS AL365441 183911 bp DNA HTG 27-JUL-2000
 DEFINITION Home sapiens chromosome 1 clone RP11-417D2, *** SEQUENCING IN
 PROGRESS ***, 11 unordred pieces.
 ACCESSION AL365441
 VERSION AL365441..4 GI:9581694
 KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE Plumb, B.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CBL01SA, UK. E-mail inquiries: humquery@sanger.ac.uk
 requests: clonerquest@sanger.ac.uk
 COMMENT On Jul 28, 2000 this sequence version replaced gi:9453777.
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA417D2
 ----- Summary Statistics
 Assembly program: XG44; version 4.5
 Sequencing vector: M13; M7815..218 of reads
 Sequencing vector: plasmid; L08752; 78% of reads
 Chemistry: Dye-terminator ABI; 33% of reads
 Chemistry: Dye-terminator Big Dye; 56% of reads
 Chemistry: Dye-primer amersham; 8% of reads
 Chemistry: Dye-primer Big Dye; 1% of reads
 Chemistry: Dye-terminator; 0% of reads
 Consensus quality: 180899 bases at least Q40
 Consensus quality: 181444 bases at least Q30
 Consensus quality: 181859 bases at least Q20
 Insert size: 183911; sum-of-contigs
 Insert size: 176659; 3.8% error; agarose-fp
 Quality coverage: 0.00% in Q20 bases; sum-of-contigs Quality coverage: 0.00% in Q20 bases; agarose-fp
 Coverage: 0.00% in Q20 bases; sum-of-contigs Quality

 * NONE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1. 5636: contig of 5636 bp in length
 * 5637 5736: gap of 100 bp
 * 5737 17994: contig of 12258 bp in length
 * 17995 18094: gap of 100 bp
 * 18095 22433: contig of 4339 bp in length
 * 22434 22531: gap of 100 bp
 * 22534 50505: contig of 27972 bp in length
 * 50505 50605: gap of 100 bp
 * 50606 65269: contig of 14664 bp in length
 * 65270 65369: gap of 100 bp
 * 65370 67875: contig of 2483 bp in length
 * 67853 67952: gap of 100 bp
 * 67953 135901: contig of 67949 bp in length
 * 135902 136001: gap of 100 bp
 * 136002 147390: contig of 11389 bp in length
 * 147391 14790: gap of 100 bp
 * 147491 151011: contig of 3521 bp in length
 * 151012 151111: gap of 100 bp
 * 151112 163809: contig of 12698 bp in length
 * 163810 163911: gap of 100 bp
 * 163910 183911: contig of 20002 bp in length.
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 /chromosome="1"
 /clone="RP1-417D2"
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 136002. .147390
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 misc_feature
 147491
 151011

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L80355
 Center clone name: 281_E_22
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.60731
 Consensus quality: 182912 bases at least Q40
 Consensus quality: 192383 bases at least Q30
 Consensus quality: 195712 bases at least Q20
 Insert size: 217000; agarose-fp
 Insert size: 199373; sum-of-contigs
 Quality coverage: 3.5 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 35 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1182: 1182: contig of 1182 bp in length
 * 1183 1282: gap of 100 bp
 * 1283 2698: contig of 1416 bp in length
 * 2699 2798: gap of 100 bp
 * 2799 4194: contig of 1396 bp in length
 * 4195 4294: gap of 100 bp
 * 4295 5704: contig of 1410 bp in length
 * 5705 5804: gap of 100 bp
 * 5805 8389: contig of 2585 bp in length
 * 8390 8489: gap of 100 bp
 * 8490 10352: contig of 1863 bp in length
 * 10353 10454: gap of 100 bp
 * 10453 13024: contig of 2572 bp in length
 * 13025 13124: gap of 100 bp
 * 13125 15709: contig of 2585 bp in length
 * 15710 15809: gap of 100 bp
 * 15810 17470: contig of 1661 bp in length
 * 17471 17570: gap of 100 bp
 * 17571 20151: contig of 2581 bp in length
 * 20152 20251: gap of 100 bp
 * 20252 22870: contig of 2619 bp in length
 * 22871 22970: gap of 100 bp
 * 22971 25709: contig of 2739 bp in length
 * 25710 25809: gap of 100 bp
 * 25810 28338: contig of 2529 bp in length
 * 28339 28438: gap of 100 bp
 * 28439 32476: contig of 4038 bp in length
 * 32477 32576: gap of 100 bp
 * 32577 37518: contig of 4942 bp in length
 * 37519 37618: gap of 100 bp
 * 37619 41724: contig of 4106 bp in length
 * 41725 41824: gap of 100 bp
 * 41825 46408: contig of 4584 bp in length
 * 46409 46509: gap of 100 bp
 * 46509 51711: contig of 5203 bp in length
 * 51712 51811: gap of 100 bp
 * 51812 56860: contig of 5049 bp in length
 * 56861 56960: gap of 100 bp
 * 56961 62871: contig of 5911 bp in length
 * 62871 62971: gap of 100 bp
 * 62972 69111: contig of 6140 bp in length
 * 69112 69211: gap of 100 bp
 * 69212 75632: contig of 6421 bp in length
 * 75633 75732: gap of 100 bp
 * 75733 81565: contig of 5833 bp in length
 * 81566 81665: gap of 100 bp
 * 81666 880181: contig of 6516 bp in length

* 88182 88285: gap of 100 bp
 * 88282 95593: contig of 7312 bp in length
 * 95594 95693: gap of 100 bp
 * 95694 103809: contig of 8116 bp in length
 * 103810 103909: gap of 8489 bp in length
 * 103910 112398: contig of 100 bp
 * 112399 112438: gap of 100 bp
 * 112499 120033: contig of 735 bp in length
 * 120034 120133: gap of 100 bp
 * 120134 12004: contig of 8871 bp in length
 * 129005 129104: gap of 100 bp
 * 129105 130574: contig of 8470 bp in length
 * 137575 137674: gap of 100 bp
 * 137675 140983: contig of 9309 bp in length
 * 140984 147093: gap of 100 bp
 * 147084 155907: contig of 9824 bp in length
 * 156908 157007: gap of 100 bp
 * 157008 163350: contig of 11343 bp in length
 * 168351 168450: gap of 100 bp
 * 168451 185212: contig of 16762 bp in length
 * 185213 185312: gap of 100 bp
 * 185313 202773: contig of 17466 bp in length

FEATURES
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misc_feature	/note="assembly_name:Contig17"	AUTHORS Kwon, B.S., Kozak, C.A., Kim, K.K. and Pickard, R.T.
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misc_feature	/note="assembly_name:Contig18"	JOURNAL J. Immunol. 152 (5), 2256-2262 (1994)
misc_feature	23139 . 27293	MEDLINE 94179B05
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misc_feature	27394 . 30127	AUTHORS Kwon, B.S.
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vector_side:left	/note="assembly_name:SP6	JOURNAL Submitted (18-Oct-1993) Kwon, B.S., Indiana University School of Medicine, Microbiology and Immunology, 635 Barnhill Dr., Indianapolis, IN 46202, USA
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Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L6087
 Center clone name: 691_A_5

----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-Terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 161108 bases at least Q40
 Consensus quality: 159789 bases at least Q30
 Consensus quality: 173200 bases at least Q20
 Insert size: 198000; agarose-fp
 Insert size: 198000; agarose-fp
 Quality coverage: 3.6 in Q20 bases; sum-of-contigs
 Quality coverage: 4.1 in Q20 bases; sum-of-contigs

 * NONE: This is a 'working draft' sequence. It currently
 * consists of 36 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

 * 1 1450; contig of 1450 bp in length
 * 1451 1550; gap of 100 bp
 * 1551 3335; contig of 1785 bp in length
 * 3336 3435; gap of 100 bp
 * 3436 4468; contig of 1033 bp in length
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* 142813 142913: gap of 100 bp
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 03:39:41 ; search time 76.15 Seconds
 (without alignments)
 4134.016 Million cell updates/sec

Title: US-08-955-572-1
 Perfect score: 838

Sequence: 1atccatggttgttagatca.....aatagggtgtggactt 838

Scoring table: IDENTITY.NUC
 Gapov 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 96044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Genesed_36:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
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4	836.4	99.8	1415	18	F91026
5	836.4	99.8	1439	20	T09769
6	831.6	99.2	838	20	Q8951
7	828.4	98.9	1439	16	Q92086
8	808.8	97.6	946	18	T8896
9	608.8	72.6	946	20	X02152
10	339.2	40.5	2347	17	T39541
11	337.6	40.3	2350	16	Q86127
12	337.6	40.3	2350	20	X90763

CC	human T-lymphocyte	leukemia	virus type-1	transformed	human T-	DT	01-APR-1998	(first entry)
CC	lymphocytes.					XX		
XX						DE	DNA	encoding a human h4-1BBSV receptor.
SQ	Sequence 1439	BP:	393	A;	336	C;	346	G;
	Best Local Similarity	99.3%	Score	828.4;	DB	16;	Length	1439;
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							Gaps	0;
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Db	100	aatcgcttgcgtatcatacgtcgccaggatccatcatggaaacgcgttaca	159					
QY	61	cattatcgccactcgttgcgtggccatcaacttgcggatggacaaatcat	120					
Db	160	cattatcgccactcgttgcgtggatggatggatggatggatggatggat	219					
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Db	220	ttgtatgtatgcgttgcgtatcatacgtcgccaggatccatcatggaa	279					
QY	181	ctgttcctcccaataatttcccgccaggatggatggatggatggatgg	240					
Db	280	ctgttcctcccaataatttcccgccaggatggatggatggatggatgg	339					
QY	241	gtgttaagggttttcaggccaggaaaggatgttccaccaatgcagatgt	300					
Db	340	gtgttaagggttttcaggccaggaaaggatgttccaccaatgcagatgt	399					
QY	301	ctgcaactccagggttcaactcgccctggccaggatgtcaggatgt	360					
Db	400	ctgcaactccagggttcaactcgccctggccaggatgtcaggatgt	459					
QY	361	acaatgtccaaacgtgacaaaaaaagggttaaagactgtgtgtgt	420					
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QY	421	tcagaacacgtggatctgtggatggatggatggatggatggatgg	480					
Db	520	tcagaacacgtggatctgtggatggatggatggatggatggatgg	579					
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XX	AC	T88969;						

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OM nucleic - nucleic search, using sw model.

Run on: November 22, 2000, 00:49:40 ; Search time 61.81 seconds
 (without alignments)

2050.483 Million cell updates/sec

Title: US-08-955-572-1
 Perfect score: 838
 Sequence: 1 aatccatggcttgatcatca.....aatagggtgtggacttt 838

Scoring table: IDENTITY.NUC
 Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Maximum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents.NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	838	100.0	838	Sequence 1, Appl1
3	836.4	99.8	1415	Sequence 7, Appl1
4	608.8	72.6	946	Sequence 7, Appl1
5	339.2	40.5	2347	Sequence 1, Appl1
6	331.4	39.5	768	Sequence 6, Appl1
7	45.6	5.4	7218	Sequence 1, Appl1
8	42.2	5.0	7218	Sequence 1, Appl1
9	35.8	4.3	3133	Sequence 1, Appl1
10	34.8	4.2	1391	Sequence 1, Appl1
11	34.8	4.2	3115	Sequence 1, Appl1
12	34.8	4.2	3136	Sequence 1, Appl1
13	3.8	723	5	Sequence 1, Appl1
14	31.4	3.7	15231	Sequence 1, Appl1
15	31.4	3.7	176373	Sequence 1, Appl1
16	31	3.7	4060	Sequence 1, Appl1
17	31	3.7	246240	Sequence 1, Appl1
18	31	3.7	246240	Sequence 1, Appl1
19	31	3.7	246240	Sequence 1, Appl1
20	30.6	3.7	291	Sequence 1, Appl1
21	30.6	3.7	291	Sequence 1, Appl1
22	30.6	3.7	291	Sequence 1, Appl1
23	30.6	3.7	291	Sequence 1, Appl1
24	30.6	3.7	291	Sequence 1, Appl1
25	30.4	3.6	12127	Sequence 1, Appl1
26	30	3.6	US-08-944-544-32	Sequence 1, Appl1

ALIGMENTS

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 ; APPLICANT: Byoung Se Kwon
 ; TITLE OF INVENTION: New Human Receptor and Related Products
 ; NUMBER OF INVENTION: and Methods
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Barnard & Brown
 ; STREET: 306 E. State St., Suite 220
 ; CITY: Ithaca
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 14850
 COMPUTER READABLE FORM:
 COMPUTER: IBM AT Compatible
 OPERATING SYSTEM: MS DOS, Version 5.0
 SOFTWARE: Special QBasic program
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/TUS94/10457
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/012,269
 FILING DATE: 2/7/93
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/932,996
 FILING DATE: 7/30/92
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/267,577
 FILING DATE: 11/7/88
 ATTORNEY/AGENT INFORMATION:
 NAME: Michaels, Christopher A.
 REGISTRATION NUMBER: 34,390
 REFERENCE/DOCKET NUMBER: kwnh4bb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 607-273-1711
 TELEFAX: 607-273-2609
 TELE:
 INFORMATION FOR SEQ ID NO: 1 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 838
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: No

Query Match 39.5%; Score 331.4; DB 1; Length 768;
 Best Local Similarity 68.2%; Pred. No. 1.9e-93; Matches 522; Conservative 0; Mismatches 231; Indels 12; Gaps 4;
 QY 671 tctgtgtttaacggggcaaaaactccgtatataatccaaacccattttataga 730
 Db 770 TCTGTCCTCAATGGATCAGGAAATACTCCACATATCAAGCACACATTAGAAG 829
 QY 731 ccagtacaactactcaagggaaatggctgtatgtcgccatgttccagaagaagaga 790
 Db 830 ACCATCGGAGCTCAAGAGGAAGATGCTGTAGCTGCCGATGTCACAGGAGANGAA 889
 QY 791 ggaggatgtgaa 802
 Db 890 GGAGGAGGAGGA 901
 RESULT 6
 US-08-236-918A-5
 ; Sequence 5, Application US/08236918A
 ; Patent No. 5574704
 ; GENERAL INFORMATION:
 ; APPLICANT: Alderson, Mark R.
 ; APPLICANT: Goodwin, Raymond G.
 ; APPLICANT: Smith, Craig A.
 ; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple 7.5.3
 ; SOFTWARE: Microsoft Word, Version #6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/08/236, 918A
 FILING DATE: 06-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/050, 843
 FILING DATE: 07-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2801-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0030
 TELEFAX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 768 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: mu4-1BB
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..768
 FEATURE:
 NAME/KEY: mat-peptide
 LOCATION: 70..768
 FEATURE:
 NAME/KEY: si-peptide
 LOCATION: 1..69
 ; US-08-236-918A-5
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPox VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; US-08-236-918A-5
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPox VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria

ADDRESSEE: CAMPBELL, AND FLORES
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States of America
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,809
 FILING DATE: 08/08/1996

CLASSIFICATION:
 514

ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 9503

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3133 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: join(3..419, 421..2858)
 US-08-162-809-1

Query Match 4.3%; Score 35.8; DB 1; Length 3133;
 Best Local Similarity 50.9%; Pred. NO. 0.24;
 Matches 85; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 120 ctgtgtactgtccatgtttctccggccatgtgtataacaggatcatgttgcgtc 179
 Db 644 CTTGAGAGCCCTCCGGCTGGACATCAAAAGCCAGTCAGGGTCGGGGCTGGTGC 703

Qy 180 ctgtgtccatgtttctccggccatgtgtataacaggatcatgttgcgtc 239
 Db 704 GCTGTCGCCACAGCGCTTCAGCGCAGGGCTTCACCGCTTGGCCCTGCCACG 763

Qy 240 agtgttaagggtttcaggaccaggaggatgttccacacgc 286
 Db 764 GCTTACTTTCGGCTGACCTGGACCGACAGTGCTGCACCCAG 810

RESULT 10
 US-08-996-139-3
 Sequence 3, Application US/08996139
 Patent No. 6017729

GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 APPLICANT: Galibert, Laurent
 APPLICANT: Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,139
 FILING DATE: 22 DECEMBER 1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 60/064,671
 FILING DATE: 14 OCTOBER 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 08/813,509
 FILING DATE: 07 MARCH 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 08/772,330
 FILING DATE: 23 DECEMBER 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0544

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1391 base pairs

FEATURE:
 NAME/KEY: CDS
 LOCATION: 9D-15C
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: HOMO SAPIENS
 IMMEDIATE SOURCE:
 LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
 CLONE:
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 39..1391
 US-08-996-139-3

Query Match 4.2%; Score 34.8; DB 5; Length 1391;
 Best Local Similarity 50.6%; Pred. NO. 0.32;
 Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 431 ggcatctgtccggccatgtgtataacaggatcatgttgcgtc 490
 Db 537 GACAAATGGAGACCCCTGGACCAACTGTAACCTCTCTGGAAAGAGATGAGACATCATGG 596

Qy 491 acgaaggaggaggatgtgtgtggacatctc 524
 Db 597 ACAGAGAAATCCGATGCCGTTGCAAGTCCTTC 630

RESULT 11
 US-08-996-139-1
 Sequence 1, Application US/08996139
 Patent No. 6017729

GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 APPLICANT: Galibert, Laurent
 APPLICANT: Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh

* Fri Nov 24 17:29:10 2000

us-08-955-572-1.rni

Db 38794 gcactctgttattactccctttatgac 38822

Search completed: November 22, 2000, 05:34:18
Job time: 17078 sec

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On nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:29:20 ; Search time 770.21 Seconds
 (without alignments)
 6726.986 Million cell updates/sec

Title: US_08-955-572-1
 Perfect score: 838
 Sequence: aatcagcttgcata...aataggctgtggactt 838

Scoring table: IDENTITY-NUC
 Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

-Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

16: gb_est16:*

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18: gb_est18:*

19: gb_est19:*

20: gb_est20:*

21: gb_est21:*

22: gb_est22:*

23: gb_est23:*

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38: gb_est38:*

39: gb_est39:*

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41: em_estba:*

42: em_estfun:*

43: em_esthml:*

44: em_esthml2:*

45: em_esthml3:*

46: em_esthml4:*

47: em_esthml5:*

48: em_esthml6:*

49: em_esthml7:*

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73: em_estpl4:*

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91: gb_gss4:*

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93: em_gss2:*

94: em_gss3:*

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96: gb_gss5:*

97: gb_gss6:*

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99: gb_gss8:*

100: gb_gss9:*

101: gb_gss10:*

102: gb_gss11:*

103: gb_gss12:*

104: gb_gss13:*

105: gb_gss14:*

106: gb_gss15:*

107: gb_gss16:*

108: gb_gss17:*

109: gb_gss18:*

110: gb_gss19:*

111: gb_gss20:*

112: gb_gss21:*

113: gb_gss22:*

114: gb_gss23:*

115: gb_gss24:*

116: em_gss5:*

Page 2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

LOCUS	BE207340	570 bp	mRNA	EST	27-JUN-2000
DEFINITION	bab11.1Y.14	Homo sapiens	CDNA clone	IMAGE:29210109	5'
		similar to gb-J04492	Mouse T-cell receptor 4-1BB protein mRNA,		
ACCESSION	BE207340	complete cds (MOUSE);	mRNA sequence.		
VERSION	BE207340.1	GI:8750738			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS	1 (bases 1 to 570)				
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.				

Result No.	Score	Query Match	Length	DB	ID	Description
1	491	58.6	570	34	BE207340	Tissue Procurement: DCTP/PP cDNA Library Preparation: Ling Hong/Rubin Laboratory
2	272	32.5	548	13	BE233113	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
3	241	28.8	610	1	AA109726	DNA Sequencing by: Washington University Genome Sequencing Center
4	235.2	28.1	687	9	AA1236084	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
5	231	27.6	674	7	AA946462	http://image.llnl.gov/html/resources.shtml
6	203.2	24.2	589	1	AA087107	Seq primer: -40RP from Gibco
7	198.6	23.7	491	12	AA1664286	High quality sequence stop: 516.
8	198.6	23.7	332	9	AA172529	Location/Qualifiers
9	58.6	7.0	330	25	AW20027	1. .570
c	10	57.4	6.8	291	11	/organism="Homo sapiens"
c	11	42.4	5.1	688	2	/ab_xref="taxon:9606"
c	12	40.2	4.8	578	5	/clone="IMAGE:294109"
c	13	39.8	4.7	529	38	/clone_1.lib="NH_MCG_14"
c	14	38.8	4.6	304	6	/tissue_type="renal cell adenocarcinoma"
c	15	38	4.5	468	104	/lab_host="BHLB (phage-resistant)"
c	16	38	4.5	573	106	/note="Organ: kidney; Vector: pOMB7; Site_1: XbaI; Site_2:
c	17	37.8	4.5	578	109	ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'
c	18	37.6	4.5	383	88	adaptor: GGCAGGAG(G). Sizes selected >500bp for average
c	19	36.6	4.4	803	112	insert size 1.8kb. Library constructed by Ling Hong in
c	20	36.2	4.3	404	24	the laboratory of Gerald M. Rubin (University of
c	21	36.2	4.3	442	6	California, Berkeley) using ZAP-cDNA synthesis kit
c	22	36	4.3	751	103	AQ819200 nb0b034I
c	23	36	4.3	1101	112	ALI07710 Drosophil
c	24	35.8	4.3	382	24	AW79644 MR2-UW002
c	25	35.8	4.3	676	109	AZ226416 RPCI-23-1
c	26	35.6	4.2	291	28	BB232607 BB232607
c	27	35.6	4.2	420	36	BE524618 M52B95M
c	28	35.4	4.2	904	108	BE524618 M52B95M
c	29	35.4	4.2	1068	115	BB232607 BB232607
c	30	35.2	4.2	417	20	ALI07710 Drosophil
c	31	35.2	4.2	504	102	AQ785579 HS_3077_A
c	32	35	4.2	375	102	AW177881 D05 Neop7
c	33	35	4.2	459	114	AL242423 Tetradon
c	34	35	4.2	1101	112	ALI01932 Drosophil
c	35	35	4.2	1101	112	ALI06956 Drosophil
c	36	35	4.2	1201	112	ALI06238 Drosophil
c	37	34.8	4.2	261	29	BB32451 BB324451
c	38	34.8	4.2	90	40	AQ218065 HS_3251_B
c	39	34.8	4.2	561	21	AW391329 QV0-ST021
c	40	34.8	4.2	562	21	AW380345 QV3-H0026
c	41	34.8	4.2	751	108	AW200704 SP_1026_A
c	42	34.6	4.1	505	5	AA613256
c	43	34.6	4.1	679	102	AQ795961 nbxb058J
c	44	34.6	4.1	1101	112	AL064052 Drosophil
c	45	34.4	4.1	1101	112	AA310644 ER3181611
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ALIGNMENTS

Db	380	CTGCACTCCAGGGTTCACTGCTGGGGCAGGATGCGACATGTGACAGCAGGTGTA	439
Qy	361	acaaggtaacaagaactgacaaaaaaagggtgtaaactgtgttggacattdaaca	420
Db	440	ACAGGTCAGAACTGACAAAAAAGGTTGTAAGACTGTGCTTGGATGAAAGTGTGCT	499
Qy	421	tcagaaactgtgtacatctgtcgacccctggacaaactgtgttggatgaaactgtgtgt	480
Db	500	TCGAAACCTGGCATCTGTGACCTTGGACAAACTGTCTTGGATGAAAGTGTGCT	559
Qy	481	tgtgaatggaa 491	
Db	560	TGTGAATGGGA 570	
RESULT	2		
BB233113	BB233113	548 bp mRNA	EST
LOCUS	139153	MARC 1PIG	Sus scrofa
DEFINITION	BE233113	5', mRNA sequence.	
ACCESSION	BE233113		
VERSION	BE233113.1	GI:9017831	
KEYWORDS	EST.		
SOURCE			
ORGANISM			
TITLE			
REFERENCE			
JOURNAL			
COMMENT			
AUTHORS			
KEYWORDS			
PIG			
Sus scrofa			
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.			
Fahrerking, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.			
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine			
EST			
Unpublished (2000)			
Contact: Smith, T.P.L.			
USA, ARS, US Meat Animal Research Center			
PO Box 166, Clay Center, NE 68933-0166, USA			
Tel: 402 762 4366			
Fax: 402 762 4390			
Email: smithe@email.marc.usda.gov			
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.			
PCR PRIMERS			
FORWARD: AGGAACAGCTATGACCAT			
BACKWARD: GTTTCACCTACCAACG			
Plate: 75			
Row: P			
Column: 5			
Seq primer: ATTTAGGAGACATATAG.			
FEATURES			
SOURCE			
Location/Qualifiers			
1. .358			
/organism="Sus scrofa"			
/db_xref="taxon:9823"			
/clone_lib="MARC 1PIG"			
/tissue_type="pooled"			
/lab_host="DH10B"			
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XbaI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."			
BASE COUNT	138	a 162 g 123 t	
ORIGIN			
Query Match	32.5%	Score 272; DB 34; Length 548;	
Best Local Similarity	73.6%	Pred. No. 2e-69; Indels 42; Gaps 1;	
Matches	381;	Conservative 0; Mismatches 95;	
Oy	311	gggttcaactgtggggcaggatgcaggatgtgtggacaaaggatctaacaaggatcaa	370
Db	38	GGATTCGGCTGCTGGGGCGGGATGCGCAAGACTATGCCAGAACGCTAA	97
Qy	371	gaacttacaaaaaaaagggtgtaaactgtgtttggacatatacgatcagaaacgt	430
Db	98	GAGTAAACCGCAAGAAGGTTGTAAGACTGTGCTTGGACATTCATGAGGACAT	157
RESULT	2		
BB233113	BB233113	548 bp mRNA	EST
LOCUS	139153	MARC 1PIG	Sus scrofa
DEFINITION	BE233113	5', mRNA sequence.	
ACCESSION	BE233113		
VERSION	BE233113.1	GI:9017831	
KEYWORDS	EST.		
SOURCE			
ORGANISM			
TITLE			
REFERENCE			
JOURNAL			
COMMENT			
AUTHORS			
KEYWORDS			
PIG			
Sus scrofa			
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.			
Fahrerking, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.			
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine			
EST			
Unpublished (2000)			
Contact: Smith, T.P.L.			
USA, ARS, US Meat Animal Research Center			
PO Box 166, Clay Center, NE 68933-0166, USA			
Tel: 402 762 4366			
Fax: 402 762 4390			
Email: smithe@email.marc.usda.gov			
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.			
PCR PRIMERS			
FORWARD: AGGAACAGCTATGACCAT			
BACKWARD: GTTTCACCTACCAACG			
Plate: 75			
Row: P			
Column: 5			
Seq primer: ATTTAGGAGACATATAG.			
FEATURES			
SOURCE			
Location/Qualifiers			
1. .358			
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/clone_lib="MARC 1PIG"			
/tissue_type="pooled"			
/lab_host="DH10B"			
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XbaI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."			
BASE COUNT	138	a 162 g 123 t	
ORIGIN			
Query Match	32.5%	Score 272; DB 34; Length 548;	
Best Local Similarity	73.6%	Pred. No. 2e-69; Indels 42; Gaps 1;	
Matches	381;	Conservative 0; Mismatches 95;	
Oy	311	gggttcaactgtggggcaggatgcaggatgtgtggacaaaggatctaacaaggatcaa	370
Db	38	GGATTCGGCTGCTGGGGCGGGATGCGCAAGACTATGCCAGAACGCTAA	97
Qy	371	gaacttacaaaaaaaagggtgtaaactgtgtttggacatatacgatcagaaacgt	430
Db	98	GAGTAAACCGCAAGAAGGTTGTAAGACTGTGCTTGGACATTCATGAGGACAT	157
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AA109726	AA109726	610 bp mRNA	EST
LOCUS	AA109726	AA109726	610 bp mRNA
DEFINITION	AA109726	mp0f11_r1 life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA clone IMAGE:568845 5' similar to qb:J04492 Mouse T-cell receptor 4 IBB protein mRNA, complete cds (MOUSE); mRNA sequence.	
ACCESSION	AA109726		
VERSION	AA109726		
KEYWORDS	EST.		
SOURCE			
ORGANISM			
TITLE			
REFERENCE			
JOURNAL			
COMMENT			
AUTHORS			
KEYWORDS			
PIG			
Sus scrofa			
Mus musculus			
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.			
Fahrerking, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.			
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine			
EST			
Unpublished (1996)			
Contact: Marra, M.			
WASHU-HMM Mouse EST Project			
Washington University School of Medicine			
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
Tel: 314 286 1800			
Fax: 314 286 1810			
Email: mouseest@wustl.edu			
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.			
MGI: 343493			
Seq primer: -28M13 rev1 from Amersham			
High quality sequence stop: 399.			
FEATURES			
SOURCE			
Location/Qualifiers			
1. .610			
/organism="Mus musculus"			
/db_xref="taxon:67"			
/clone="C57BL/6J"			
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"			
/tissue_type="embryo"			
/dev_stage="8 5dpc embryos"			
/lab_host="DH10B"			

ORIGIN BASE COUNT
Sail; Site_2: NotI; Cloned undirectionally. Primer:
Oligo dT. 8.5Dpc embryos. PCMV-SPORT2 vector. "a"
139 a 146 c 175 g 150 t

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-5329
Fax: (301)-838-0208

FEATURES	seq	primer	Location/Qualifiers
source			Location: M13-21.
	1..687		/organism="Rattus sp." /db_xref="ATCC (inbost):2042770" /db_xref="taxon:10118" /clone="ROVDB31" /clone_1.lib="Normalized rat ovary, Bento Soares" /note="Organ: ovary; Vector: pRT3pac; Site_1: ECORI; Site_2: NotI"
BASE COUNT	149 a 189 c 180 g	169 t	ORIGIN

LOCUS	EST232646	687	bp	mRNA	EST	31-JAN-1999
DEFINITION	Normalized rat ovary, Bento Sores Rattus sp. cDNA clone					
ACCESSION	EST232646	3'		end, mRNA sequence.		
VERSION	A1236084					
KEYWORDS	A1236084.1					
SOURCE	EST					
ORGANISM	Rattus	sp.				
	Rattus	sp.				
	Bukiyota					
	Metazoa					
	Chordata					
	Craniata					
	Vertebrata					
	Euteleostomi					
	Mammalia					
	Eutheria					
	Rodentia					
	Sciurognathi					
	Muridae					
	Murinae					
REFERENCE	Rattus					
AUTHORS	1					
	(bases 1 to 687)					
TITLE	Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.					
JOURNAL	Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index					
COMMENT	unpublished (1998)					
	Other_ESTs: T660155					
	Contact: Lee, NH					
	ATCC					

QY 373 a-cttacaaaaaaagggtgttaaagactttgtgtttggacatttaacatcgaaacg-- 429
 Db 413 AGCTAACGAGCAGGGTCACAAACCTGAGCTTGGACATTTAATGCCAGAGCGGA 472
 QY 430 tggatctgtcgccctgtgacaactgtgttttgatgtgaaactgtgtgtgtgtgaaatgg 489
 Db 473 GGTGTTCTGTCGACCTTGGCAGGGTGGCTCTATTCTTATAGTCTGNGC-TAAGACCGG 531
 QY 490 gaaaggagggagggacgtgggtctgtggacc 519
 Db 532 GACCGGAGAAGGACGCGTGTGTTGGACC 561

RESULT 7
 AI664286 491 bp mRNA EST 10-MAY-1999
 REFERENCE AI664286 491 bp mRNA EST 10-MAY-1999
 LOCUS AI664286 491 bp mRNA EST 10-MAY-1999
 AUTHORS 1. bases 1 to 491
 TITLE NC-I-CAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph. D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available through LInL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI: 935357

Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 419.

FEATURES source
 1. .491
 /organism="Mus musculus"
 /ab_xref="taxon:10090"
 /clone="IMGR:149753"
 /clone_libr="Soares_NMPL"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pRTT3D-Pac (Pharmacia) with
 a modified polylinker; 1st strand cDNA was prepared from
 pregnant mouse uterus, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was linearized to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pRTT3
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo. #
 BASE COUNT 114 a 118 c 135 g 124 t
 ORIGIN

Query Match 23.7%; Score 198.6; DB 12; length 491;
 Best local similarity 68.0%; Pred No. 8.9e-48;
 Matches 308; Conservative 0; Mismatches 139; Indels 6; Gaps 2;

QY 13 tagttatccatccgtgcagatccatcatggaaacacgtgttacatgtggcc 72
 Db 41 TGGTGTCTGTCATGTCATGCCATGGAAACACTGTTACAACGTTGGTGTCT 100
 QY 73 tctgtgtgtggtcactcaacttggagggacaatcatgtggatccatgtggactg 132
 Db 101 TGGTGTCTGTCATGGGGTCGAGAAGGTGGGCCAGACTCTGTGAACTG 160
 QY 133 cccagctgttacattctgtgataataacacggaaatccatcgttgcagtccctgtcccaa 192

RESULT 8
 AI172529 332 bp mRNA EST 05-JUL-1999
 REFERENCE AI172529 332 bp mRNA EST 05-JUL-1999
 AUTHORS 1. bases 1 to 332
 TITLE UI-R-C2P-nu-g-01-0-UI s1 UI-R-C2P Rattus norvegicus cDNA clone
 ACCESION AI172529
 JOURNAL AI172529.1 GI:3712569
 VERSION EST
 KEYWORDS SOURCE
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Rattus.
 REFERENCE AI172529 332 bp mRNA EST 05-JUL-1999
 AUTHORS 1. bases 1 to 332
 TITLE UI-R-C2P-nu-g-01-0-UI s1 UI-R-C2P Rattus norvegicus cDNA clone
 ACCESION AI172529
 JOURNAL AI172529.1 GI:3712569
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Echstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@weeg.uiowa.edu
 The sequence tag present in the cDNA between the NotI site and the
 oligo-dT track served to identify it as a clone from the normalized
 adult Ovary library. cDNA Library Preparation: M. Fatima Bonaldo,
 Ph.D. Clone distribution: clones will be available through Research
 Genetics. This clone is also available through the I.M.A.G.E.
 Consortium at LInL (info@image.llnl.gov). IMAGE ID:178664. The
 following repetitive elements were found in this cDNA sequence:
 1-37, >AT-rich#low_complexity
 Seq primer: M13 Forward
 POLYA>No.

FEATURES source
 1. .332
 /location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /ab_xref="taxon:10116"
 /clone="UI-R-C2P-nu-g-01-0-UI"
 /clone_libr="UI-R-C2P"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="vector: pRTT3D-Pac (Pharmacia) with a modified
 polylinker; Site-1: Not I; Site-2: Eco RI; The UI-R-C2P
 library is a subtracted library derived from the UI-R-C2P
 library, which is a subtracted library derived from the

UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2P) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESNs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxypatite column chromatography, converted to double stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2P library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).¹

BASE COUNT

71 a

75 c

76 g

109 t

1 others

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```
 /lab_host="SOLR (kanamycin resistant)" /host="Osmann, Linda, Vector, plasmid" /w=1 /size=1 /report=1
```

[5'-TGT TACCA ATCT GAGT GGGGCC CAATT TTTTTTTT TTTT-3'],

/node: ORIGIN: long; vector: bluescript SK-; SITES: ECOLI; Site_2: XbaI; Cloned unidirectionally. PRIMER: Oligo GT 3', Bulk lung tumor. 5' adaptor sequence: 5' GAATTGGCAGAG 3', 3' adaptor sequence: 5' ctcGAGTTTTTTTTTTTTTTT 3', Average insert size: 1.1 kb." ORIGIN BASE COUNT 150 a 164 c 164 g 100 t

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR3 vector (Pharmacia). Library went through one round of normalization to a $C_0 = 5$. Library constructed by Bento Soares and M. Ratina Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHHL99.

Query Match	4.8%	Score 40.2;	DB 5;	Length 578;
Best Local Similarity	50.8%	Pred. No. 0.55;	DB 5;	Length 578;
Matches	96;	Conservative	0;	Mismatches 93; Indels 0; Gaps 0;
Qy	482	gtgaatggagaatggaggaggacgtgttctgtgaccatctcagtcgtacccctctcgg	541	
Db	473	GTAGATGGTCCATGGCAAGAGGAGAGTAAAGGGCTCCCTCCCTGGCTCGAG	414	
Qy	542	ggagccatctgtgaccccctcgccctcgagagaggacactccgcagatc	601	
Db	413	CTGGCTTCCACCTGGACGCGCCTGCTGCTTCCTGAGAGCCGGCCCTCCCTCAGTAC	354	
Qy	602	atctccatcttcgtcgatcgatcgatcgatgttcgttcgtgttcgttcgttcgt	661	
Db	353	TCTGTTGGCCCTCTGCTTCCCCATTCCTCCACAGCTCATAGCTCGTACATCTG	294	
Qy	662	atcccgttc	670	
Db	293	GCCTCTGTC	285	

RESULT 13

ACCESSION [2] PIR:SA4279 ; mRNA Sequence.
VERSION N8001
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 529)

AUTHORS
 Hillier,L., Clark,M., Dubuque,T., Ellison,K., Hawkins,M., Holman,
 'M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mara,M., Parsons,J.,
 Rifkin,L., Ronfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,
 'R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE
 The Waslu-Merck EST Project
JOURNAL
 Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LInL; contact the
IMAGE Consortium (image.llnl.gov) for further information.
Seq primer: m13-40 forward
High quality sequence stop: 316.

Qy 662 ctccggttc 6700
Db 288 GCCCTTGTC 2800

RESULT 14

LOCUS BB290438 304 bp mRNA EST 09-JUL-2000
DEFINITION BB290438 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
ALIAS BB290438-31, similar to M0402, mouse "M-51" connector-4-1bp

ACCESSION
VERSTON
BB290433
RS290433 1 GT-R90987
protein mRNA, mRNA sequence.

KEYWORDS
EST.
house mouse.
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 304)

AUTHORS
Kondo, H., Aizawa, K., Akhuria, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

, T., Suzuki, H., Tagawa, A., Takayanagi, T., Tomiyama, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamakata, I., Yano, R., Yasunari, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Miyamoto, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Konno, H., et al.)
JOURNAL Unpublished
COMMENT Contact Yoshihide Hayashizaki

```

organism="Homo sapiens"
/DB_XREF="GDB:1246259"
/db_xref="txon:9606"
/clone="IMAGE:301335"
/clone.lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab.host="D110B (ampicillin resistant)"
/note="Organ: lung; Vector: pMT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer

```

Genome Exploration Research Group, Life Science Tsukuba Center,
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Sciences Center
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@tc.riken.go.jp/
URL: <http://genome.tc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,

